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LETTER TO THE EDITOR

A case of pulmonary *Mycobacterium celatum* in an Indian AIDS patient

Mycobacterium celatum was first described in 1993 as a new mycobacterial species biochemically indistinguishable from the *Mycobacterium avium—intracellulare* complex (MAC), with a mycolic acid pattern closely related to that of *Mycobacterium xenopi*.[1]

The infections caused by this organism were reported to occur mostly in people with suppressed cell-mediated immunity, such as AIDS patients[2—4] but infections also occurred in apparently immunocompetent hosts. In India the most common mycobacterial co-infection in AIDS patients is reported to be *Mycobacterium tuberculosis*. But so far no case of *Mycobacterium celatum* infection has been reported from this part of the world, even though infection with *M. celatum* is classified as an AIDS-associated opportunistic infection.[3,4] This is probably due to a lack of technical infrastructure which is necessary to correctly speciate the isolates. This correspondence reports the first case of *Mycobacterium celatum* in an Indian AIDS patient. The isolate was speciated using both biochemical and 16S rRNA PCR-sequencing methods.

In 1997 a 24-year-old female was found to be HIV positive and remained asymptomatic until 2001 when she was referred to us with complaints of fever, weight loss, breathlessness and purulent but scant expectoration. Her husband had died of AIDS-associated pulmonary tuberculosis. On examination she was emaciated, dyspneic, and in poor general condition. Her chest X-ray showed apical cavitary lesions with hilar shadows. Her Mantoux test was 15 mm (negative $<$10 mm in diameter) with 10 purified TU. Her biochemical parameters showed mildly raised liver enzymes, an erythrocyte sedimentation rate of 39 mm for the first hour, and haemoglobin 8 g/dl. She tested HIV-1 positive. Her CD4+/CD8+ counts were 120 and 990 cells/μl, respectively.

Her three consecutive sputum samples were sent to the laboratory and two of the these were both smear and culture positive for *Mycobacterium* spp. Both the isolates were identified biochemically as *M. avium—intracellulare* complex. Drug susceptibility of the isolates showed resistance to isoniazid and rifampicin, but sensitivity for ethambutol and ciprofloxacin. This led us to further characterize the isolates under an ongoing project on molecular characterization of multidrug-resistant (MDR) strains. The PCR was performed using 30 pmol of primer 264 (5′ TGC ACA CAG GCC ACA AGG GA 3′; corresponding to *Escherichia coli* 16S rRNA from position 1046 to 1027), and 30 pmol of primer 285 (5′GAG AGT TTG ATC CTG GCT CAG 3′; corresponding to *E. coli* 16S rRNA from position 9 to 30). The PCR products were further purified (Qiagen® USA) and sequenced using the sequencing primer 244 (5′ CCC ACT GCT GCC TCC CGT AG 3′) and primer 259 (5′ TTT CAC GAA CAA CGC GAC AA 3′) for determining the nucleic acid sequence of the hypervariable region B. The sequence data was aligned and BLAST® searched, which confirmed these isolates as *M. celatum*. The sequence data is submitted to GenBank with accession no—AF504926.

In recent years, several other clinically important mycobacterial species have been identified internationally.[2—5] However, in Indian AIDS patients, *Mycobacterium tuberculosis* infection is reported to be the leading opportunistic infection. It is possible that in India several non-tubercular species of *Mycobacterium* are underreported and remain unidentified due to inadequate laboratory facilities. Most Indian laboratories use conventional phenotypic methods, which have poor inter-species discriminatory power. Since this species biochemically closely resembles *M. avium-intracelluare* complex, it can only be correctly identified by molecular techniques such as 16S rRNA gene sequencing.[2—5] The isolate could have been mis-identified as *M. avium-intracelluare* complex had molecular methods not been applied.

The present report of a pulmonary infection with *M. celatum* indicates that mycobacterial isolates from immunocompromised patients must be identified to species level using modern molecular tools. A correct and rapid diagnosis may be crucial, not only

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for documentation but also for successfully treating the infection. The clinical presentation of the case reported here was indistinguishable from that of *M. tuberculosis* infection and in resource-limited settings where tuberculosis is endemic, these cases are very likely to be missed.

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